

RAW SEQUENCE LISTING

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Application Serial Number: 08/252,384D
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RAW SEQUENCE LISTING

DATE: 03/07/2007

PATENT APPLICATION: US/08/252,384D

TIME: 15:04:39

Input Set : N:\efs\03_07_07\08252384D_efs\RACT00100.txt

Output Set: N:\CRF4\03062007\H252384D.raw

Use

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3 <110> APPLICANT: Reactive Surfaces, Ltd.
4     McDaniel, Steven
5     Raushel, Frank M
6     Wild, James R
8 <120> TITLE OF INVENTION: Recombinant Organophosphorous Acid Anhydrase and Methods of
Use
10 <130> FILE REFERENCE: TAMK145
12 <140> CURRENT APPLICATION NUMBER: US 08/252,384D
13 <141> CURRENT FILING DATE: 1994-06-01
15 <150> PRIOR APPLICATION NUMBER: US 07/928,540
16 <151> PRIOR FILING DATE: 1992-08-13
18 <150> PRIOR APPLICATION NUMBER: US 07/344,258
19 <151> PRIOR FILING DATE: 1989-04-27
21 <160> NUMBER OF SEQ ID NOS: 4
23 <170> SOFTWARE: PatentIn version 3.3
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1337
27 <212> TYPE: DNA
28 <213> ORGANISM: Pseudomonas diminuta
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (63)..(1160)
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39 Met Gln Thr Arg Arg Val Val Leu Lys Ser Ala Ala Ala Gly
40 1 5 10 15
42 act ctg ctc ggc ggc ctg gct ggg tgc gcg agc gtg gct gga tcg atc      155
43 Thr Leu Leu Gly Gly Leu Ala Gly Cys Ala Ser Val Ala Gly Ser Ile
44 20 25 30
46 ggc aca ggc gat cgg atc aat acc gtg cgc ggt cct atc aca atc tct      203
47 Gly Thr Gly Asp Arg Ile Asn Thr Val Arg Gly Pro Ile Thr Ile Ser
48 35 40 45
50 gaa gcg ggt ttc aca ctg act cac gag cac atc tgc ggc agc tcg gca      251
51 Glu Ala Gly Phe Thr Leu Thr His Glu His Ile Cys Gly Ser Ser Ala
52 50 55 60
54 gga ttc ttg cgt gct tgg cca gag ttc ttc ggt agc cgc aaa gct cta      299
55 Gly Phe Leu Arg Ala Trp Pro Glu Phe Phe Gly Ser Arg Lys Ala Leu
56 65 70 75
58 gcg gaa aag gct gtg aga gga ttg cgc cgc gcc aga gcg gct ggc gtg      347
59 Ala Glu Lys Ala Val Arg Gly Leu Arg Arg Ala Arg Ala Ala Gly Val
60 80 85 90 95
62 cga acg att gtc gat gtg tcg act ttc gat atc ggt cgc gac gtc agt      395
63 Arg Thr Ile Val Asp Val Ser Thr Phe Asp Ile Gly Arg Asp Val Ser

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67	Leu Leu Ala Glu Val Ser Arg Ala Ala Asp Val His Ile Val Ala Ala						
68		115		120		125	
70	acc ggc ttg tgg ttc gac ccg cca ctt tcg atg cga ttg agg agt gta						491
71	Thr Gly Leu Trp Phe Asp Pro Pro Leu Ser Met Arg Leu Arg Ser Val						
72		130		135		140	
74	gag gaa ctc aca cag ttc ttc ctg cgt gag att caa tat ggc atc gaa						539
75	Glu Glu Leu Thr Gln Phe Phe Leu Arg Glu Ile Gln Tyr Gly Ile Glu						
76		145		150		155	
78	gac acc gga att agg gcg ggc att atc aag gtc gcg acc aca ggc aag						587
79	Asp Thr Gly Ile Arg Ala Gly Ile Ile Lys Val Ala Thr Thr Gly Lys						
80	160		165		170		175
82	gcg acc ccc ttt cag gag tta gtg tta aag gcg gcc gcc ccg gcc agc						635
83	Ala Thr Pro Phe Gln Glu Leu Val Leu Lys Ala Ala Ala Arg Ala Ser						
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86	ttg gcc acc ggt gtt ccg gta acc act cac acg gca gca agt cag cgc						683
87	Leu Ala Thr Gly Val Pro Val Thr Thr His Thr Ala Ala Ser Gln Arg						
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91	Asp Gly Glu Gln Gln Ala Ala Ile Phe Glu Ser Glu Gly Leu Ser Pro						
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94	tca cgg gtt tgt att ggt cac agc gat gat act gac gat ttg agc tat						779
95	Ser Arg Val Cys Ile Gly His Ser Asp Asp Thr Asp Asp Leu Ser Tyr						
96		225		230		235	
98	ctc acc gcc ctc gct gcg cgc gga tac ctc atc ggt cta gac cac atc						827
99	Leu Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu Asp His Ile						
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102	ccg cac agt gcg att ggt cta gaa gat aat gcg agt gca tca gcc ctc						875
103	Pro His Ser Ala Ile Gly Leu Glu Asp Asn Ala Ser Ala Ser Ala Leu						
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110	atc gac caa ggc tac atg aaa caa atc ctc gtt tcg aat gac tgg ctg						971
111	Ile Asp Gln Gly Tyr Met Lys Gln Ile Leu Val Ser Asn Asp Trp Leu						
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115	Phe Gly Phe Ser Ser Tyr Val Thr Asn Ile Met Asp Val Met Asp Arg						
116		305		310		315	
118	gtg aac ccc gac ggg atg gcc ttc att cca ctg aga gtg atc cca ttc						1067
119	Val Asn Pro Asp Gly Met Ala Phe Ile Pro Leu Arg Val Ile Pro Phe						
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122	cta cga gag aag ggc gtc cca cag gaa acg ctg gca ggc atc act gtg						1115
123	Leu Arg Glu Lys Gly Val Pro Gln Glu Thr Leu Ala Gly Ile Thr Val						
124		340		345		350	
126	act aac ccg gcg cgg ttc ttg tca ccg acc ttg ccg gcg tca tga						1160
127	Thr Asn Pro Ala Arg Phe Leu Ser Pro Thr Leu Arg Ala Ser						
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139 <212> TYPE: PRT
140 <213> ORGANISM: Pseudomonas diminuta
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149 20 25 30
152 Thr Gly Asp Arg Ile Asn Thr Val Arg Gly Pro Ile Thr Ile Ser Glu
153 35 40 45
156 Ala Gly Phe Thr Leu Thr His Glu His Ile Cys Gly Ser Ser Ala Gly
157 50 55 60
160 Phe Leu Arg Ala Trp Pro Glu Phe Phe Gly Ser Arg Lys Ala Leu Ala
161 65 70 75 80
164 Glu Lys Ala Val Arg Gly Leu Arg Arg Ala Arg Ala Ala Gly Val Arg
165 85 90 95
168 Thr Ile Val Asp Val Ser Thr Phe Asp Ile Gly Arg Asp Val Ser Leu
169 100 105 110
172 Leu Ala Glu Val Ser Arg Ala Ala Asp Val His Ile Val Ala Ala Thr
173 115 120 125
176 Gly Leu Trp Phe Asp Pro Pro Leu Ser Met Arg Leu Arg Ser Val Glu
177 130 135 140
180 Glu Leu Thr Gln Phe Phe Leu Arg Glu Ile Gln Tyr Gly Ile Glu Asp
181 145 150 155 160
184 Thr Gly Ile Arg Ala Gly Ile Ile Lys Val Ala Thr Thr Gly Lys Ala
185 165 170 175
188 Thr Pro Phe Gln Glu Leu Val Leu Lys Ala Ala Ala Arg Ala Ser Leu
189 180 185 190
192 Ala Thr Gly Val Pro Val Thr Thr His Thr Ala Ala Ser Gln Arg Asp
193 195 200 205
196 Gly Glu Gln Gln Ala Ala Ile Phe Glu Ser Glu Gly Leu Ser Pro Ser
197 210 215 220
200 Arg Val Cys Ile Gly His Ser Asp Asp Thr Asp Asp Leu Ser Tyr Leu
201 225 230 235 240
204 Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu Asp His Ile Pro
205 245 250 255
208 His Ser Ala Ile Gly Leu Glu Asp Asn Ala Ser Ala Ser Ala Leu Leu
209 260 265 270
212 Gly Ile Arg Ser Trp Gln Thr Arg Ala Leu Leu Ile Lys Ala Leu Ile
213 275 280 285
216 Asp Gln Gly Tyr Met Lys Gln Ile Leu Val Ser Asn Asp Trp Leu Phe
217 290 295 300
220 Gly Phe Ser Ser Tyr Val Thr Asn Ile Met Asp Val Met Asp Arg Val
221 305 310 315 320
224 Asn Pro Asp Gly Met Ala Phe Ile Pro Leu Arg Val Ile Pro Phe Leu

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250 Met Gln Thr Arg Arg Val Val Leu Lys Ser Ala Ala Ala Gly Thr
251 1 5 10 15
253 ctg ctc ggc ggc ctg gct ggg tgc gcg acg tgg ctg gat cga tcg gca 155
254 Leu Leu Gly Gly Leu Ala Gly Cys Ala Thr Trp Leu Asp Arg Ser Ala
255 20 25 30
257 cag gcg atc gga tca ata cgt gcg cgt cct atc aca atc tct gaa gcg 203
258 Gln Ala Ile Gly Ser Ile Arg Ala Arg Pro Ile Thr Ile Ser Glu Ala
259 35 40 45
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262 Gly Phe Thr Leu Thr His Glu Asp Ile Cys Gly Ser Ser Ala Gly Phe
263 50 55 60
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266 Leu Arg Ala Trp Pro Glu Phe Phe Gly Ser Arg Lys Ala Leu Ala Glu
267 65 70 75
269 aag gct gtg aga gga ttg cgc gcc aga gcg gct ggc gtg cga acg att 347
270 Lys Ala Val Arg Gly Leu Arg Ala Arg Ala Ala Gly Val Arg Thr Ile
271 80 85 90 95
273 gtc gat gtg tgc act ttc gat atc ggt cgc gac gtc agt tta ttg gcc 395
274 Val Asp Val Ser Thr Phe Asp Ile Gly Arg Asp Val Ser Leu Leu Ala
275 100 105 110
277 gag gtt tgc cgg gct gcc gac gtt cat atc gtg gcg gcg acc ggc ttg 443
278 Glu Val Ser Arg Ala Ala Asp Val His Ile Val Ala Ala Thr Gly Leu
279 115 120 125
281 tgg ttc gac ccg cca ctt tgc atg cga ttg agg tat gta gag gaa ctc 491
282 Trp Phe Asp Pro Pro Leu Ser Met Arg Leu Arg Tyr Val Glu Glu Leu
283 130 135 140
285 aca cag ttc ttc ctg cgt gag att caa tat ggc atc gaa gac acc gga 539
286 Thr Gln Phe Phe Leu Arg Glu Ile Gln Tyr Gly Ile Glu Asp Thr Gly
287 145 150 155
289 att agg gcg ggc att atc aag gtc gcg acc aca ggc aag gcg acc ccc 587
290 Ile Arg Ala Gly Ile Ile Lys Val Ala Thr Thr Gly Lys Ala Thr Pro
291 160 165 170 175
293 ttt cag gag tta gtg tta aag gcg gcc gcc cgg gcc agc ttg gcc acc 635
294 Phe Gln Glu Leu Val Leu Lys Ala Ala Ala Arg Ala Ser Leu Ala Thr

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295          180          185          190
297 ggt gtt ccg gta acc act cac acg gca gca agt cag cgc gat ggt gag      683
298 Gly Val Pro Val Thr Thr His Thr Ala Ala Ser Gln Arg Asp Gly Glu
299          195          200          205
301 cga ggc agg ccg cca ttt ttg agt ccg aag ctt gag ccc tca cgg gtt      731
302 Arg Gly Arg Pro Pro Phe Leu Ser Pro Lys Leu Glu Pro Ser Arg Val
303          210          215          220
305 tgt att ggt cac agc gat gat act gac gat ttg agc tat ctc acc gcc      779
306 Cys Ile Gly His Ser Asp Asp Thr Asp Asp Leu Ser Tyr Leu Thr Ala
307          225          230          235
309 ctg ctg cgc gga tac ctc atc ggt cta gac cac atc ccg cac agt gcg      827
310 Leu Leu Arg Gly Tyr Leu Ile Gly Leu Asp His Ile Pro His Ser Ala
311 240          245          250          255
313 att ggt cta gaa gat aat gcg agt gca tca ccg ctc ctg ggc atc cgt      875
314 Ile Gly Leu Glu Asp Asn Ala Ser Ala Ser Pro Leu Leu Gly Ile Arg
315          260          265          270
317 tcg tgg caa aca cgg gct ctc ttg atc aag gcg ctc atc gac caa ggc      923
318 Ser Trp Gln Thr Arg Ala Leu Leu Ile Lys Ala Leu Ile Asp Gln Gly
319          275          280          285
321 tac atg aaa caa atc ctc gtt tcg aat gac tgg ctg ttc ggg ttt tcg      971
322 Tyr Met Lys Gln Ile Leu Val Ser Asn Asp Trp Leu Phe Gly Phe Ser
323          290          295          300
325 agc tat gtc acc aac atc atg gac gtg atg gat cgc gtg aac ccc gac      1019
326 Ser Tyr Val Thr Asn Ile Met Asp Val Met Asp Arg Val Asn Pro Asp
327          305          310          315
329 ggg atg gcc ttc att cca ctg aga gtg atc cca ttc tac gag aga agg      1067
330 Gly Met Ala Phe Ile Pro Leu Arg Val Ile Pro Phe Tyr Glu Arg Arg
331 320          325          330          335
333 gcg tcc cac agg aaa cgc tgc cag gca tca ctg tgactaacc cgcgcggttc      1120
334 Ala Ser His Arg Lys Arg Cys Gln Ala Ser Leu
335          340          345
337 tgtgtcaccg acttgctgg atgtcacgcc atctggatcc ttccagccag cggccactat      1180
339 tccccgtcaa gataccgaac gatgaagtcg cgcacgcgac gataggcatc ttcaattgtg      1240
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346 <210> SEQ ID NO: 4
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358          20          25          30
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362          35          40          45
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VERIFICATION SUMMARY

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